

SEQUENCE LISTING

<110> Evologic S.A.

Maliere Technologies Société Civile

Rhodia Chimie

Marliere, Phillipe

<120> Cloning of gluconate dehydratase gcuD gene

<130> G 3111 EP

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 1812

<212> DNA

<213> Agrobacterium tumefaciens

<220>

<221> CDS

<222> (1)..(1809)

<223>

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cgc gcc tgg ttc gac aac cca gcc aat gcg gac atg acc gcg ctt tat	96
Arg Ala Trp Phe Asp Asn Pro Ala Asn Ala Asp Met Thr Ala Leu Tyr	
20 25 30	
ctc gag cgt tac atg aac ttc ggt ctc agc cag gcc gag ctt cag tcc	144
Leu Glu Arg Tyr Met Asn Phe Gly Leu Ser Gln Ala Glu Leu Gln Ser	

35	40	45	
gac cgc ccg att atc ggt att gcg cag acc ggt tcc gac ctt tcg ccc			192
Asp Arg Pro Ile Ile Gly Ile Ala Gln Thr Gly Ser Asp Leu Ser Pro			
50	55	60	
tgc aac cgt cat cat ctg gaa ctc gcc aac cgt ctg cgt gaa ggc att			240
Cys Asn Arg His His Leu Glu Leu Ala Asn Arg Leu Arg Glu Gly Ile			
65	70	75	80
cgt gaa gcc ggc ggc atc gcc atc gaa ttc ccg gtg cat ccg atc cag			288
Arg Glu Ala Gly Gly Ile Ala Ile Glu Phe Pro Val His Pro Ile Gln			
	85	90	95
gaa acc ggt aag cgt ccg aca gcg ggc ctt gat cgc aac ctg gct tac			336
Glu Thr Gly Lys Arg Pro Thr Ala Gly Leu Asp Arg Asn Leu Ala Tyr			
	100	105	110
ctc ggc ctc gtg gaa gtg ctt tat ggc tat ccg ctc gac ggc gtt gtt			384
Leu Gly Leu Val Glu Val Leu Tyr Gly Tyr Pro Leu Asp Gly Val Val			
	115	120	125
ctg acc atc ggc tgc gac aag acc acg cct gcc tgt ctt atg gcg gcg			432
Leu Thr Ile Gly Cys Asp Lys Thr Thr Pro Ala Cys Leu Met Ala Ala			
	130	135	140
gcc acc gtc aac att ccg gcc atc gcc ctt tcc gtc ggt ccc atg ctg			480
Ala Thr Val Asn Ile Pro Ala Ile Ala Leu Ser Val Gly Pro Met Leu			
	145	150	155
aac ggc tgg ttc cgc ggt gag cgc acc ggt tcc ggc acc atc gtc tgg			528
Asn Gly Trp Phe Arg Gly Glu Arg Thr Gly Ser Gly Thr Ile Val Trp			
	165	170	175
aag gcc cgc gaa ctg ctg gcg aag ggc gag atc gat tac cag ggc ttc			576
Lys Ala Arg Glu Leu Leu Ala Lys Gly Glu Ile Asp Tyr Gln Gly Phe			
	180	185	190
gtc aag ctc gtt gcc tcg tct gcc ccg tcc acc ggc tat tgc aac acc			624
Val Lys Leu Val Ala Ser Ser Ala Pro Ser Thr Gly Tyr Cys Asn Thr			
	195	200	205
atg ggc acg gca aca acc atg aac tcg ctc gcc gaa gcg ctc ggc atg			672
Met Gly Thr Ala Thr Thr Met Asn Ser Leu Ala Glu Ala Leu Gly Met			
	210	215	220
cag ctt ccc ggc tcc gcc gcc att ccg gcg cct tac cgt gac cgt cag			720
Gln Leu Pro Gly Ser Ala Ala Ile Pro Ala Pro Tyr Arg Asp Arg Gln			
	225	230	235
gaa gtc tct tac ctc acc ggc ctg cgc atc gtc gac atg gtc agg gaa			768
Glu Val Ser Tyr Leu Thr Gly Leu Arg Ile Val Asp Met Val Arg Glu			
	245	250	255
gac ctg aaa cca tca gac atc atg acc aag gat gcc ttc atc aac gcc			816
Asp Leu Lys Pro Ser Asp Ile Met Thr Lys Asp Ala Phe Ile Asn Ala			
	260	265	270
atc cgc gtt aat tcg gcg atc ggc ggt tcc acc aac gcg ccg atc cat			864
Ile Arg Val Asn Ser Ala Ile Gly Gly Ser Thr Asn Ala Pro Ile His			

275	280	285	
cta aac ggc ctt gcc cgc cat gtc ggc gtc gag ctg acg gtg gat gac Leu Asn Gly Leu Ala Arg His Val Gly Val Glu Leu Thr Val Asp Asp 290 295 300			912
tgg cag acc tat ggc gaa gac gtg ccg ctg ctc gtc aac ctg cag ccg Trp Gln Thr Tyr Gly Glu Asp Val Pro Leu Val Asn Leu Gln Pro 305 310 315 320			960
gca ggc gaa tat ctc ggc gag gac tat tac cat gcc ggc ggc gtt ccc Ala Gly Glu Tyr Leu Gly Glu Asp Tyr Tyr His Ala Gly Gly Val Pro 325 330 335			1008
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aac cct gat gat ccg gaa gcc ttc gaa ggc cgc gcc gtg gtg ttc gat Asn Pro Asp Asp Pro Glu Ala Phe Glu Gly Arg Ala Val Val Phe Asp 420 425 430			1296
ggt ccg gag gat tac cat cat cgc atc gac gat ccg tcg ctt ggc atc Gly Pro Glu Asp Tyr His His Arg Ile Asp Asp Pro Ser Leu Gly Ile 435 440 445			1344
gac gcc aac acc gtc ctg ttc atg cgc ggc gcc ggt ccg atc ggt tac Asp Ala Asn Thr Val Leu Phe Met Arg Gly Ala Gly Pro Ile Gly Tyr 450 455 460			1392
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gcc ggc ggc ggt ctg tct att ctg cag acg ggt gac cgc gtc cgc atc			1584

Ala Gly Gly Gly Leu Ser Ile Leu Gln Thr Gly Asp Arg Val Arg Ile
 515 520 525
 gat gtg ggc cgc ggc aag gcc gat atc ctg ata tca ggt gaa gag ctc 1632
 Asp Val Gly Arg Gly Lys Ala Asp Ile Leu Ile Ser Gly Glu Glu Leu
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 gcc aag cgt tac gag gcg ctg gca gct cag gcc ggt tat aag ttc ccc 1680
 Ala Lys Arg Tyr Glu Ala Leu Ala Ala Gln Gly Gly Tyr Lys Phe Pro
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 gac cac cag acg ccg tgg cag gaa atc cag cgc ggt atc gtc agc cag 1728
 Asp His Gln Thr Pro Trp Gln Glu Ile Gln Arg Gly Ile Val Ser Gln
 565 570 575
 atg gaa acc ggc gcg gtt ctg gaa ccg gcc gta aag tat cag cgc atc 1776
 Met Glu Thr Gly Ala Val Leu Glu Pro Ala Val Lys Tyr Gln Arg Ile
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 gcc cag acc aag ggc ctg ccg cgc gat aac cac tga 1812
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<210> 2

<211> 603

<212> PRT

<213> Agrobacterium tumefaciens

<400> 2

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 Leu Glu Arg Tyr Met Asn Phe Gly Leu Ser Gln Ala Glu Leu Gln Ser
 35 40 45
 Asp Arg Pro Ile Ile Gly Ile Ala Gln Thr Gly Ser Asp Leu Ser Pro
 50 55 60
 Cys Asn Arg His His Leu Glu Leu Ala Asn Arg Leu Arg Glu Gly Ile
 65 70 75 80
 Arg Glu Ala Gly Gly Ile Ala Ile Glu Phe Pro Val His Pro Ile Gln
 85 90 95

Glu Thr Gly Lys Arg Pro Thr Ala Gly Leu Asp Arg Asn Leu Ala Tyr
 100 105 110

Leu Gly Leu Val Glu Val Leu Tyr Gly Tyr Pro Leu Asp Gly Val Val
 115 120 125

Leu Thr Ile Gly Cys Asp Lys Thr Thr Pro Ala Cys Leu Met Ala Ala
 130 135 140

Ala Thr Val Asn Ile Pro Ala Ile Ala Leu Ser Val Gly Pro Met Leu
 145 150 155 160

Asn Gly Trp Phe Arg Gly Glu Arg Thr Gly Ser Gly Thr Ile Val Trp
 165 170 175

Lys Ala Arg Glu Leu Leu Ala Lys Gly Glu Ile Asp Tyr Gln Gly Phe
 180 185 190

Val Lys Leu Val Ala Ser Ser Ala Pro Ser Thr Gly Tyr Cys Asn Thr
 195 200 205

Met Gly Thr Ala Thr Thr Met Asn Ser Leu Ala Glu Ala Leu Gly Met
 210 215 220

Gln Leu Pro Gly Ser Ala Ala Ile Pro Ala Pro Tyr Arg Asp Arg Gln
 225 230 235 240

Glu Val Ser Tyr Leu Thr Gly Leu Arg Ile Val Asp Met Val Arg Glu
 245 250 255

Asp Leu Lys Pro Ser Asp Ile Met Thr Lys Asp Ala Phe Ile Asn Ala
 260 265 270

Ile Arg Val Asn Ser Ala Ile Gly Gly Ser Thr Asn Ala Pro Ile His
 275 280 285

Leu Asn Gly Leu Ala Arg His Val Gly Val Glu Leu Thr Val Asp Asp
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Trp Gln Thr Tyr Gly Glu Asp Val Pro Leu Leu Val Asn Leu Gln Pro
 305 310 315 320

Ala Gly Glu Tyr Leu Gly Glu Asp Tyr Tyr His Ala Gly Gly Val Pro
 325 330 335

Ala Val Val Asn Gln Leu Met Thr Gln Gly Leu Ile Met Glu Asp Ala
 340 345 350

Met Thr Val Asn Gly Lys Thr Ile Gly Asp Asn Cys Arg Gly Ala Ile
 355 360 365

Ile Glu Asp Glu Lys Val Ile Arg Pro Tyr Glu Gln Pro Leu Lys Glu
 370 375 380

Arg Ala Gly Phe Arg Val Leu Arg Gly Asn Leu Phe Ser Ser Ala Ile
 385 390 395 400

Met Lys Thr Ser Val Ile Ser Glu Glu Phe Arg Gly Arg Tyr Leu Ser
 405 410 415

Asn Pro Asp Asp Pro Glu Ala Phe Glu Gly Arg Ala Val Val Phe Asp
 420 425 430

Gly Pro Glu Asp Tyr His His Arg Ile Asp Asp Pro Ser Leu Gly Ile
 435 440 445

Asp Ala Asn Thr Val Leu Phe Met Arg Gly Ala Gly Pro Ile Gly Tyr
 450 455 460

Pro Gly Ala Ala Glu Val Val Asn Met Arg Ala Pro Asp Tyr Leu Leu
 465 470 475 480

Lys Gln Gly Val Ser Ser Leu Pro Cys Ile Gly Asp Gly Arg Gln Ser
 485 490 495

Gly Thr Ser Gly Ser Pro Ser Ile Leu Asn Ala Ser Pro Glu Ala Ala
 500 505 510

Ala Gly Gly Gly Leu Ser Ile Leu Gln Thr Gly Asp Arg Val Arg Ile
 515 520 525

Asp Val Gly Arg Gly Lys Ala Asp Ile Leu Ile Ser Gly Glu Glu Leu
 530 535 540

Ala Lys Arg Tyr Glu Ala Leu Ala Ala Gln Gly Gly Tyr Lys Phe Pro
 545 550 555 560

Asp His Gln Thr Pro Trp Gln Glu Ile Gln Arg Gly Ile Val Ser Gln

565

570

575

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Ala Gln Thr Lys Gly Leu Pro Arg Asp Asn His
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<211> 1272

<212> DNA

<213> Agrobacterium tumefaciens

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<221> CDS

<222> (1)..(1269)

<223>

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 Tyr His Ala Gln Ser Asn Met Ile Gly Ser Ser Pro Ala Asp Gly Leu
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ctc gca ttg ccg ctt ctg acc gtc gat ctt gcc gtc tat cgc ggt aat 144
 Leu Ala Leu Pro Leu Leu Thr Val Asp Leu Ala Val Tyr Arg Gly Asn
 35 40 45

cgg gat cgc ttt ctt gcg ctt gtc tcg gcc cat gga gcg aag gcg gct 192
 Arg Asp Arg Phe Leu Ala Leu Val Ser Ala His Gly Ala Lys Ala Ala
 50 55 60

cca cat gcc aag acg ccg atg tgc ccg gag atc gcg atc gat ctg att 240
 Pro His Ala Lys Thr Pro Met Cys Pro Glu Ile Ala Ile Asp Leu Ile
 65 70 75 80

gaa gcc ggt gcc tgg ggc gcg acg gtc gcc gat ctc ttc cag gcg gaa 288
 Glu Ala Gly Ala Trp Gly Ala Thr Val Ala Asp Leu Phe Gln Ala Glu
 85 90 95

gtc ctg ctc aag gcc ggc gtg tcg aac ata ttg atc gcc aac cag atc 336
 Val Leu Leu Lys Ala Gly Val Ser Asn Ile Leu Ile Ala Asn Gln Ile
 100 105 110

ggc gga ttg aca tcc gcc aga cgc cta cgc atg ctc gca gat gct ttt Gly Gly Leu Thr Ser Ala Arg Arg Leu Arg Met Leu Ala Asp Ala Phe 115 120 125	384
ccg aaa gcc gag att atc tgc tgt gtc gat tct gtt cag gcc tcg gcc Pro Lys Ala Glu Ile Ile Cys Cys Val Asp Ser Val Gln Ala Ser Ala 130 135 140	432
aat ctg gtt cag gcc ttt caa ggg cgt gtg gat gcc cca ttc aag gtc Asn Leu Val Gln Ala Phe Gln Gly Arg Val Asp Ala Pro Phe Lys Val 145 150 155 160	480
ttc atc gaa gtc ggt gtc gcc cgc act ggc gcc cgt acg ttg aat gtt Phe Ile Glu Val Gly Val Gly Arg Thr Gly Ala Arg Thr Leu Asn Val 165 170 175	528
gca aag gat atc atc gac acc atc tcg aca agt gca gaa atc gta ctg Ala Lys Asp Ile Ile Asp Thr Ile Ser Thr Ser Ala Glu Ile Val Leu 180 185 190	576
gcc ggt gtg tcg acc tat gaa ggc tcc gtc tcc ggg gaa acg tcg gaa Ala Gly Val Ser Thr Tyr Glu Gly Ser Val Ser Gly Glu Thr Ser Glu 195 200 205	624
gca ctc gat gca aac atg gcg gcc ctg ttc gat ctc ctg acc gac agt Ala Leu Asp Ala Asn Met Ala Ala Leu Phe Asp Leu Leu Thr Asp Ser 210 215 220	672
ctt gca tcg ata cgc gaa aaa gat ccc ggg cgc ccg cta acg gtt tca Leu Ala Ser Ile Arg Glu Lys Asp Pro Gly Arg Pro Leu Thr Val Ser 225 230 235 240	720
gcc ggc ggt tcg atc cat ttc gac cgc gtg ctc gcg gcg ctt gtg ccc Ala Gly Gly Ser Ile His Phe Asp Arg Val Leu Ala Ala Leu Val Pro 245 250 255	768
gtt tgc gag gcg gat ggc aat gcg acg ttg ttg ctg cgc agc ggc gcc Val Cys Glu Ala Asp Gly Asn Ala Thr Leu Leu Leu Arg Ser Gly Ala 260 265 270	816
atc ttc ttc tct gat cac ggt gta tat cag cgc ggt ttc cag gca gtc Ile Phe Phe Ser Asp His Gly Val Tyr Gln Arg Gly Phe Gln Ala Val 275 280 285	864
gac gcc cgc aac cta ctc gca tcc gcc aag gtt gtc ttc aag gca tcc Asp Ala Arg Asn Leu Leu Ala Ser Gly Lys Val Val Phe Lys Ala Ser 290 295 300	912
gag gca ttt cag ccc tca atg cga atc tgg gcg gag gtc atc tcc gtt Glu Ala Phe Gln Pro Ser Met Arg Ile Trp Ala Glu Val Ile Ser Val 305 310 315 320	960
cct gag ccg ggg ctg gcg atc gtc gcc atg gcc atg ccg gat gta tcg Pro Glu Pro Gly Leu Ala Ile Val Gly Met Gly Met Arg Asp Val Ser 325 330 335	1008
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340 345 350
 ctg gtc gaa gct gat ctc tct tca tcc gcg aag gtc ggc aag ctc aat 1104
 Leu Val Glu Ala Asp Leu Ser Ser Ser Ala Lys Val Gly Lys Leu Asn
 355 360 365
 gac cag cat gcc ttc ttg tcc ttc ggg aac ggc agc agt ctg gca atc 1152
 Asp Gln His Ala Phe Leu Ser Phe Gly Asn Gly Ser Ser Leu Ala Ile
 370 375 380
 ggc gat gtc ata gaa ttc ggc atc tcg cat ccc tgc acg tgc ttc gat 1200
 Gly Asp Val Ile Glu Phe Gly Ile Ser His Pro Cys Thr Cys Phe Asp
 385 390 395 400
 cgc tgg cgc gtc ttt cac gga atc gat gga tca ggc cgg atc cag cgc 1248
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 Ile Tyr Thr Thr Phe Phe His
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 <213> Agrobacterium tumefaciens
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 Arg Asp Arg Phe Leu Ala Leu Val Ser Ala His Gly Ala Lys Ala Ala
 50 55 60
 Pro His Ala Lys Thr Pro Met Cys Pro Glu Ile Ala Ile Asp Leu Ile
 65 70 75 80
 Glu Ala Gly Ala Trp Gly Ala Thr Val Ala Asp Leu Phe Gln Ala Glu
 85 90 95

Val Leu Leu Lys Ala Gly Val Ser Asn Ile Leu Ile Ala Asn Gln Ile
 100 105 110

Gly Gly Leu Thr Ser Ala Arg Arg Leu Arg Met Leu Ala Asp Ala Phe
 115 120 125

Pro Lys Ala Glu Ile Ile Cys Cys Val Asp Ser Val Gln Ala Ser Ala
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Asn Leu Val Gln Ala Phe Gln Gly Arg Val Asp Ala Pro Phe Lys Val
 145 150 155 160

Phe Ile Glu Val Gly Val Gly Arg Thr Gly Ala Arg Thr Leu Asn Val
 165 170 175

Ala Lys Asp Ile Ile Asp Thr Ile Ser Thr Ser Ala Glu Ile Val Leu
 180 185 190

Ala Gly Val Ser Thr Tyr Glu Gly Ser Val Ser Gly Glu Thr Ser Glu
 195 200 205

Ala Leu Asp Ala Asn Met Ala Ala Leu Phe Asp Leu Leu Thr Asp Ser
 210 215 220

Leu Ala Ser Ile Arg Glu Lys Asp Pro Gly Arg Pro Leu Thr Val Ser
 225 230 235 240

Ala Gly Gly Ser Ile His Phe Asp Arg Val Leu Ala Ala Leu Val Pro
 245 250 255

Val Cys Glu Ala Asp Gly Asn Ala Thr Leu Leu Leu Arg Ser Gly Ala
 260 265 270

Ile Phe Phe Ser Asp His Gly Val Tyr Gln Arg Gly Phe Gln Ala Val
 275 280 285

Asp Ala Arg Asn Leu Leu Ala Ser Gly Lys Val Val Phe Lys Ala Ser
 290 295 300

Glu Ala Phe Gln Pro Ser Met Arg Ile Trp Ala Glu Val Ile Ser Val
 305 310 315 320

Pro Glu Pro Gly Leu Ala Ile Val Gly Met Gly Met Arg Asp Val Ser
 325 330 335

Phe Asp Gln Asp Leu Pro Val Ala Leu Arg Leu His Arg Asp Gly His
 340 345 350

Leu Val Glu Ala Asp Leu Ser Ser Ser Ala Lys Val Gly Lys Leu Asn
 355 360 365

Asp Gln His Ala Phe Leu Ser Phe Gly Asn Gly Ser Ser Leu Ala Ile
 370 375 380

Gly Asp Val Ile Glu Phe Gly Ile Ser His Pro Cys Thr Cys Phe Asp
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Arg Trp Arg Val Phe His Gly Ile Asp Gly Ser Gly Arg Ile Gln Arg
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Ile Tyr Thr Thr Phe Phe His
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<213> artificial sequence

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agatcgctga gataggtgcc tcaactgatta agcattggta actgtcagac caagtttact	1080
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ccggcatccg cttacagaca agctgtgacc gtctccggga gctgcatgtg tcagagggtt	2640
tcaccgtcat caccgaaacg cgca	2665

<210> 15

<211> 3433

<212> DNA

<213> vector

<400> 15

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cggccgcgga tccagatctc atcaccatca ccatcactaa gcttaattag ctgagcttgg	180
actcctgttg atagatccag taatgacctc agaactccat ctggatttgt tcagaacgct	240
cggttgccgc cgggcgtttt ttattggtga gaatccaagc tagcttggcg agattttcag	300
gagctaagga agctaaaatg gagaaaaaaa tctactggata taccaccgtt gatatatccc	360
aatggcatcg taaagaacat tttagggcat ttcagtcagt tgctcaatgt acctataacc	420
agaccgttca gctggatatt acggcctttt taaagaccgt aaagaaaaat aagcacaagt	480
tttatccggc ctttattcac attcttgccc gcctgatgaa tgctcatccg gaatttcgta	540
tggcaatgaa agacggtgag ctggtgatat gggatagtgt tcacccttgt tacaccgttt	600
tccatgagca aactgaaacg ttttcatcgc tctggagtga ataccacgac gatttccggc	660
agtttctaca catatattcg caagatgtgg cgtgttacgg tgaaaacctg gcctatttcc	720
ctaaaggggt tatttgagaat atgtttttcg tctcagccaa tccctgggtg agtttcacca	780
gttttgattt aaacgtggcc aatatggaca acttcttcgc ccccgtttcc accatgggca	840
aatattatac gcaaggcgac aaggtgctga tgccgctggc gattcagggt catcatgccg	900
tttgtgatgg cttccatgtc ggcagaatgc ttaatgaatt acaacagtac tgcgatgagt	960
ggcagggcgg ggcgtaattt ttttaaggca gttattggtg cccttaaacg cctggggtaa	1020
tgactctcta gcttgaggca tcaaataaaa cgaaaggctc agtcgaaaga ctgggccttt	1080
cgttttatct gttgtttgtc ggtgaacgct ctctgagta ggacaaatcc gccctctaga	1140
gctgcctcgc gcgtttcggg gatgacgggtg aaaacctctg acacatgcag ctcccggaga	1200
cggtcacagc ttgtctgtaa gcggatgccg ggagcagaca agcccgtcag ggcgcgtcag	1260
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gctcactgac tcgctgcgct cggtcgttcg gctgcggcga gcggtatcag ctcaactcaa	1500
ggcggtaata cggttatcca cagaatcagg ggataacgca ggaaagaaca tgtgagcaaa	1560
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 tgccgcaaaa aagggaataa gggcgacacg gaaatgttga atactcatatc tcttcctttt 3240
 tcaatattat tgaagcattt atcagggtta ttgtctcatg agcggatata tatttgaatg 3300
 tatttagaaa aataaataa taggggttcc gcgcacattt ccccgaaaag tgccacctga 3360
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ctttcgtctt cac

3433

<210> 16

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 16

atatttaatt aatgtctgaa attactttgg

30

<210> 17

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 17

atatgcggcc gcttattgct tagcggttggt

30

<210> 18

<211> 1707

<212> DNA

<213> *Zymomonas mobilis*

<220>

<221> CDS

<222> (1)..(1707)

<223>

<400> 18		
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Met Ser Tyr Thr Val Gly Thr Tyr Leu Ala Glu Arg Leu Val Gln Ile		
1 5 10 15		
ggt ctc aag cat cac ttc gca gtc gcg ggc gac tac aac ctc gtc ctt		96
Gly Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu		
20 25 30		
ctt gac aac ctg ctt ttg aac aaa aac atg gag cag gtt tat tgc tgt		144
Leu Asp Asn Leu Leu Leu Asn Lys Asn Met Glu Gln Val Tyr Cys Cys		
35 40 45		
aac gaa ctg aac tgc ggt ttc agt gca gaa ggt tat gct cgt gcc aaa		192
Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ala Lys		
50 55 60		
ggc gca gca gca gcc gtc gtt acc tac agc gtc ggt gcg ctt tcc gca		240
Gly Ala Ala Ala Ala Val Val Thr Tyr Ser Val Gly Ala Leu Ser Ala		
65 70 75 80		
ttt gat gct atc ggt ggc gcc tat gca gaa aac ctt ccg gtt atc ctg		288
Phe Asp Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu		
85 90 95		
atc tcc ggt gct ccg aac aac aat gat cac gct gct ggt cac gtg ttg		336
Ile Ser Gly Ala Pro Asn Asn Asn Asp His Ala Ala Gly His Val Leu		
100 105 110		
cat cac gct ctt ggc aaa acc gac tat cac tat cag ttg gaa atg gcc		384
His His Ala Leu Gly Lys Thr Asp Tyr His Tyr Gln Leu Glu Met Ala		
115 120 125		
aag aac atc acg gcc gcc gct gaa gcg att tac acc ccg gaa gaa gct		432
Lys Asn Ile Thr Ala Ala Ala Glu Ala Ile Tyr Thr Pro Glu Glu Ala		
130 135 140		
ccg gct aaa atc gat cac gtg att aaa act gct ctt cgt gag aag aag		480
Pro Ala Lys Ile Asp His Val Ile Lys Thr Ala Leu Arg Glu Lys Lys		
145 150 155 160		
ccg gtt tat ctc gaa atc gct tgc aac att gct tcc atg ccc tgc gcc		528
Pro Val Tyr Leu Glu Ile Ala Cys Asn Ile Ala Ser Met Pro Cys Ala		
165 170 175		
gct cct gga ccg gca agc gca ttg ttc aat gac gaa gcc agc gac gaa		576
Ala Pro Gly Pro Ala Ser Ala Leu Phe Asn Asp Glu Ala Ser Asp Glu		
180 185 190		
gct tct ttg aat gca gcg gtt gaa gaa acc ctg aaa ttc atc gcc aac		624
Ala Ser Leu Asn Ala Ala Val Glu Glu Thr Leu Lys Phe Ile Ala Asn		
195 200 205		
cgc gac aaa gtt gcc gtc ctc gtc ggc agc aag ctg cgc gca gct ggt		672
Arg Asp Lys Val Ala Val Leu Val Gly Ser Lys Leu Arg Ala Ala Gly		
210 215 220		
gct gaa gaa gct gct gtc aaa ttt gct gat gct ctc ggt ggc gca gtt		720

Ala Glu Glu Ala Ala Val Lys Phe Ala Asp Ala Leu Gly Gly Ala Val	
225	230
	235
	240
gct acc atg gct gct gca aaa agc ttc ttc cca gaa gaa aac ccg cat	768
Ala Thr Met Ala Ala Lys Ser Phe Phe Pro Glu Glu Asn Pro His	
245	250
	255
tac atc ggc acc tca tgg ggt gaa gtc agc tat ccg ggc gtt gaa aag	816
Tyr Ile Gly Thr Ser Trp Gly Glu Val Ser Tyr Pro Gly Val Glu Lys	
260	265
	270
acg atg aaa gaa gcc gat gcg gtt atc gct ctg gct cct gtc ttc aac	864
Thr Met Lys Glu Ala Asp Ala Val Ile Ala Leu Ala Pro Val Phe Asn	
275	280
	285
gac tac tcc acc act ggt tgg acg gat att cct gat cct aag aaa ctg	912
Asp Tyr Ser Thr Thr Gly Trp Thr Asp Ile Pro Asp Pro Lys Lys Leu	
290	295
	300
gtt ctc gct gaa ccg cgt tct gtc gtc gtt aac ggc att cgc ttc ccc	960
Val Leu Ala Glu Pro Arg Ser Val Val Val Asn Gly Ile Arg Phe Pro	
305	310
	315
	320
agc gtc cat ctg aaa gac tat ctg acc cgt ttg gct cag aaa gtt tcc	1008
Ser Val His Leu Lys Asp Tyr Leu Thr Arg Leu Ala Gln Lys Val Ser	
325	330
	335
aag aaa acc ggt gca ttg gac ttc ttc aaa tcc ctc aat gca ggt gaa	1056
Lys Lys Thr Gly Ala Leu Asp Phe Phe Lys Ser Leu Asn Ala Gly Glu	
340	345
	350
ctg aag aaa gcc gct ccg gct gat ccg agt gct ccg ttg gtc aac gca	1104
Leu Lys Lys Ala Ala Pro Ala Asp Pro Ser Ala Pro Leu Val Asn Ala	
355	360
	365
gaa atc gcc cgt cag gtc gaa gct ctt ctg acc ccg aac acg acg gtt	1152
Glu Ile Ala Arg Gln Val Glu Ala Leu Leu Thr Pro Asn Thr Thr Val	
370	375
	380
att gct gaa acc ggt gac tct tgg ttc aat gct cag cgc atg aag ctc	1200
Ile Ala Glu Thr Gly Asp Ser Trp Phe Asn Ala Gln Arg Met Lys Leu	
385	390
	395
	400
ccg aac ggt gct cgc gtt gaa tat gaa atg cag tgg ggt cac att ggt	1248
Pro Asn Gly Ala Arg Val Glu Tyr Glu Met Gln Trp Gly His Ile Gly	
405	410
	415
tgg tcc gtt cct gcc gcc ttc ggt tat gcc gtc ggt gct ccg gaa cgt	1296
Trp Ser Val Pro Ala Ala Phe Gly Tyr Ala Val Gly Ala Pro Glu Arg	
420	425
	430
cgc aac atc ctc atg gtt ggt gat ggt tcc ttc cag ctg acg gct cag	1344
Arg Asn Ile Leu Met Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln	
435	440
	445
gaa gtc gct cag atg gtt cgc ctg aaa ctg ccg gtt atc atc ttc ttg	1392
Glu Val Ala Gln Met Val Arg Leu Lys Leu Pro Val Ile Ile Phe Leu	
450	455
	460

atc aat aac tat ggt tac acc atc gaa gtt atg atc cat gat ggt ccg 1440
 Ile Asn Asn Tyr Gly Tyr Thr Ile Glu Val Met Ile His Asp Gly Pro
 465 470 475 480
 tac aac aac atc aag aac tgg gat tat gcc ggt ctg atg gaa gtg ttc 1488
 Tyr Asn Asn Ile Lys Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe
 485 490 495
 aac ggt aac ggt ggt tat gac agc ggt gct ggt aaa ggc ctg aag gct 1536
 Asn Gly Asn Gly Gly Tyr Asp Ser Gly Ala Gly Lys Gly Leu Lys Ala
 500 505 510
 aaa acc ggt ggc gaa ctg gca gaa gct atc aag gtt gct ctg gca aac 1584
 Lys Thr Gly Gly Glu Leu Ala Glu Ala Ile Lys Val Ala Leu Ala Asn
 515 520 525
 acc gac ggc cca acc ctg atc gaa tgc ttc atc ggt cgt gaa gac tgc 1632
 Thr Asp Gly Pro Thr Leu Ile Glu Cys Phe Ile Gly Arg Glu Asp Cys
 530 535 540
 act gaa gaa ttg gtc aaa tgg ggt aag cgc gtt gct gcc gcc aac agc 1680
 Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser
 545 550 555 560
 cgt aag cct gtt aac aag ctc ctc tag
 Arg Lys Pro Val Asn Lys Leu Leu 1707
 565

<210> 19

<211> 568

<212> PRT

<213> Zymomonas mobilis

<400> 19

Met Ser Tyr Thr Val Gly Thr Tyr Leu Ala Glu Arg Leu Val Gln Ile
 1 5 10 15
 Gly Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu
 20 25 30
 Leu Asp Asn Leu Leu Leu Asn Lys Asn Met Glu Gln Val Tyr Cys Cys
 35 40 45
 Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ala Lys
 50 55 60
 Gly Ala Ala Ala Ala Val Val Thr Tyr Ser Val Gly Ala Leu Ser Ala
 65 70 75 80

23/46

Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser
 545 550 555 560

Arg Lys Pro Val Asn Lys Leu Leu
 565

<210> 20

<211> 1692

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1692)

<223>

<400> 20

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Met Ser Glu Ile Thr Leu Gly Lys Tyr Leu Phe Glu Arg Leu Lys Gln	
1 5 10 15	
gtc aac gtt aac acc gtt ttc ggt ttg cca ggt gac ttc aac ttg tcc	96
Val Asn Val Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser	
20 25 30	
ttg ttg gac aag atc tac gaa gtt gaa ggt atg aga tgg gct ggt aac	144
Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Met Arg Trp Ala Gly Asn	
35 40 45	
gcc aac gaa ttg aac gct gct tac gcc gct gat ggt tac gct cgt atc	192
Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile	
50 55 60	
aag ggt atg tct tgt atc atc acc acc ttc ggt gtc ggt gaa ttg tct	240
Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser	
65 70 75 80	
gct ttg aac ggt att gcc ggt tct tac gct gaa cac gtc ggt gtt ttg	288
Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu	
85 90 95	
cac gtt gtt ggt gtc cca tcc atc tct gct caa gct aag caa ttg ttg	336
His Val Val Gly Val Pro Ser Ile Ser Ala Gln Ala Lys Gln Leu Leu	
100 105 110	
ttg cac cac acc ttg ggt aac ggt gac ttc act gtt ttc cac aga atg	384
Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met	

115	120	125	
tct gcc aac att tct gaa acc act gct atg atc act gac att gct acc Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Ala Thr 130 135 140			432
gcc cca gct gaa att gac aga tgt atc aga acc act tac gtc acc caa Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Val Thr Gln 145 150 155 160			480
aga cca gtc tac tta ggt ttg cca gct aac ttg gtc gac ttg aac gtc Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val 165 170 175			528
cca gct aag ttg ttg caa act cca att gac atg tct ttg aag cca aac Pro Ala Lys Leu Leu Gln Thr Pro Ile Asp Met Ser Leu Lys Pro Asn 180 185 190			576
gat gct gaa tcc gaa aag gaa gtc att gac acc atc ttg gct ttg gtc Asp Ala Glu Ser Glu Lys Glu Val Ile Asp Thr Ile Leu Ala Leu Val 195 200 205			624
aag gat gct aag aac cca gtt atc ttg gct gat gct tgt tgt tcc aga Lys Asp Ala Lys Asn Pro Val Ile Leu Ala Asp Ala Cys Cys Ser Arg 210 215 220			672
cac gac gtc aag gct gaa act aag aag ttg att gac ttg act caa ttc His Asp Val Lys Ala Glu Thr Lys Lys Leu Ile Asp Leu Thr Gln Phe 225 230 235 240			720
cca gct ttc gtc acc cca atg ggt aag ggt tcc att gac gaa caa cac Pro Ala Phe Val Thr Pro Met Gly Lys Gly Ser Ile Asp Glu Gln His 245 250 255			768
cca aga tac ggt ggt gtt tac gtc ggt acc ttg tcc aag cca gaa gtt Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Lys Pro Glu Val 260 265 270			816
aag gaa gcc gtt gaa tct gct gac ttg att ttg tct gtc ggt gct ttg Lys Glu Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Val Gly Ala Leu 275 280 285			864
ttg tct gat ttc aac acc ggt tct ttc tct tac tct tac aag acc aag Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys 290 295 300			912
aac att gtc gaa ttc cac tcc gac cac atg aag atc aga aac gcc act Asn Ile Val Glu Phe His Ser Asp His Met Lys Ile Arg Asn Ala Thr 305 310 315 320			960
ttc cca ggt gtc caa atg aaa ttc gtt ttg caa aag ttg ttg acc act Phe Pro Gly Val Gln Met Lys Phe Val Leu Gln Lys Leu Leu Thr Thr 325 330 335			1008
att gct gac gcc gct aag ggt tac aag cca gtt gct gtc cca gct aga Ile Ala Asp Ala Ala Lys Gly Tyr Lys Pro Val Ala Val Pro Ala Arg 340 345 350			1056
act cca gct aac gct gct gtc cca gct tct acc cca ttg aag caa gaa			1104

Thr	Pro	Ala	Asn	Ala	Ala	Val	Pro	Ala	Ser	Thr	Pro	Leu	Lys	Gln	Glu	
	355						360					365				
tgg	atg	tgg	aac	caa	ttg	ggg	aac	ttc	ttg	caa	gaa	ggg	gat	gtt	gtc	1152
Trp	Met	Trp	Asn	Gln	Leu	Gly	Asn	Phe	Leu	Gln	Glu	Gly	Asp	Val	Val	
	370					375					380					
att	gct	gaa	acc	ggg	acc	tcc	gct	ttc	ggg	atc	aac	caa	acc	act	ttc	1200
Ile	Ala	Glu	Thr	Gly	Thr	Ser	Ala	Phe	Gly	Ile	Asn	Gln	Thr	Thr	Phe	
	385				390					395					400	
cca	aac	aac	acc	tac	ggg	atc	tct	caa	gtc	tta	tgg	ggg	tcc	att	ggg	1248
Pro	Asn	Asn	Thr	Tyr	Gly	Ile	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly	
				405				410						415		
ttc	acc	act	ggg	gct	acc	ttg	ggg	gct	gct	ttc	gct	gct	gaa	gaa	att	1296
Phe	Thr	Thr	Gly	Ala	Thr	Leu	Gly	Ala	Ala	Phe	Ala	Ala	Glu	Glu	Ile	
			420				425						430			
gat	cca	aag	aag	aga	gtt	atc	tta	ttc	att	ggg	gac	ggg	tct	ttg	caa	1344
Asp	Pro	Lys	Lys	Arg	Val	Ile	Leu	Phe	Ile	Gly	Asp	Gly	Ser	Leu	Gln	
		435				440						445				
ttg	act	gtt	caa	gaa	atc	tcc	acc	atg	atc	aga	tgg	ggc	ttg	aag	cca	1392
Leu	Thr	Val	Gln	Glu	Ile	Ser	Thr	Met	Ile	Arg	Trp	Gly	Leu	Lys	Pro	
	450					455					460					
tac	ttg	ttc	gtc	ttg	aac	aac	gat	ggg	tac	acc	att	gaa	aag	ttg	att	1440
Tyr	Leu	Phe	Val	Leu	Asn	Asn	Asp	Gly	Tyr	Thr	Ile	Glu	Lys	Leu	Ile	
	465				470				475						480	
cac	ggg	cca	aag	gct	caa	tac	aac	gaa	att	caa	ggg	tgg	gac	cac	cta	1488
His	Gly	Pro	Lys	Ala	Gln	Tyr	Asn	Glu	Ile	Gln	Gly	Trp	Asp	His	Leu	
				485				490						495		
tcc	ttg	ttg	cca	act	ttc	ggg	gct	aag	gac	tat	gaa	acc	cac	aga	gtc	1536
Ser	Leu	Leu	Pro	Thr	Phe	Gly	Ala	Lys	Asp	Tyr	Glu	Thr	His	Arg	Val	
			500					505					510			
gct	acc	acc	ggg	gaa	tgg	gac	aag	ttg	acc	caa	gac	aag	tct	ttc	aac	1584
Ala	Thr	Thr	Gly	Glu	Trp	Asp	Lys	Leu	Thr	Gln	Asp	Lys	Ser	Phe	Asn	
		515					520					525				
gac	aac	tct	aag	atc	aga	atg	att	gaa	atc	atg	ttg	cca	gtc	ttc	gat	1632
Asp	Asn	Ser	Lys	Ile	Arg	Met	Ile	Glu	Ile	Met	Leu	Pro	Val	Phe	Asp	
	530					535					540					
gct	cca	caa	aac	ttg	gtt	gaa	caa	gct	aag	ttg	act	gct	gct	acc	aac	1680
Ala	Pro	Gln	Asn	Leu	Val	Glu	Gln	Ala	Lys	Leu	Thr	Ala	Ala	Thr	Asn	
	545				550				555						560	
gct	aag	caa	taa													1692
Ala	Lys	Gln														

<210> 21

<211> 563

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 21

Met Ser Glu Ile Thr Leu Gly Lys Tyr Leu Phe Glu Arg Leu Lys Gln
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 20 25 30
 Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Met Arg Trp Ala Gly Asn
 35 40 45
 Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile
 50 55 60
 Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser
 65 70 75 80
 Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu
 85 90 95
 His Val Val Gly Val Pro Ser Ile Ser Ala Gln Ala Lys Gln Leu Leu
 100 105 110
 Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
 115 120 125
 Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Ala Thr
 130 135 140
 Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Val Thr Gln
 145 150 155 160
 Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val
 165 170 175
 Pro Ala Lys Leu Leu Gln Thr Pro Ile Asp Met Ser Leu Lys Pro Asn
 180 185 190
 Asp Ala Glu Ser Glu Lys Glu Val Ile Asp Thr Ile Leu Ala Leu Val
 195 200 205

Lys Asp Ala Lys Asn Pro Val Ile Leu Ala Asp Ala Cys Cys Ser Arg
 210 215 220

His Asp Val Lys Ala Glu Thr Lys Lys Leu Ile Asp Leu Thr Gln Phe
 225 230 235 240

Pro Ala Phe Val Thr Pro Met Gly Lys Gly Ser Ile Asp Glu Gln His
 245 250 255

Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Lys Pro Glu Val
 260 265 270

Lys Glu Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Val Gly Ala Leu
 275 280 285

Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
 290 295 300

Asn Ile Val Glu Phe His Ser Asp His Met Lys Ile Arg Asn Ala Thr
 305 310 315 320

Phe Pro Gly Val Gln Met Lys Phe Val Leu Gln Lys Leu Leu Thr Thr
 325 330 335

Ile Ala Asp Ala Ala Lys Gly Tyr Lys Pro Val Ala Val Pro Ala Arg
 340 345 350

Thr Pro Ala Asn Ala Ala Val Pro Ala Ser Thr Pro Leu Lys Gln Glu
 355 360 365

Trp Met Trp Asn Gln Leu Gly Asn Phe Leu Gln Glu Gly Asp Val Val
 370 375 380

Ile Ala Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Thr Phe
 385 390 395 400

Pro Asn Asn Thr Tyr Gly Ile Ser Gln Val Leu Trp Gly Ser Ile Gly
 405 410 415

Phe Thr Thr Gly Ala Thr Leu Gly Ala Ala Phe Ala Ala Glu Glu Ile
 420 425 430

Asp Pro Lys Lys Arg Val Ile Leu Phe Ile Gly Asp Gly Ser Leu Gln

435

440

445

Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Lys Pro
 450 455 460

Tyr Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Leu Ile
 465 470 475 480

His Gly Pro Lys Ala Gln Tyr Asn Glu Ile Gln Gly Trp Asp His Leu
 485 490 495

Ser Leu Leu Pro Thr Phe Gly Ala Lys Asp Tyr Glu Thr His Arg Val
 500 505 510

Ala Thr Thr Gly Glu Trp Asp Lys Leu Thr Gln Asp Lys Ser Phe Asn
 515 520 525

Asp Asn Ser Lys Ile Arg Met Ile Glu Ile Met Leu Pro Val Phe Asp
 530 535 540

Ala Pro Gln Asn Leu Val Glu Gln Ala Lys Leu Thr Ala Ala Thr Asn
 545 550 555 560

Ala Lys Gln

<210> 22

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 22

tctttaatta atgggttgtc cgtcattcat ata

33

<210> 23

<211> 32

<212> DNA

<213> . artificial sequence

<220>

<223> artificial sequence

<400> 23

ctaaagcttt taggccagag tggctcttgcg cg

32

<210> 24

<211> 1674

<212> DNA

<213> *Acetobacter pasteurianus*

<220>

<221> CDS

<222> (1)..(1674)

<223>

<400> 24

gtg acc tat act gtt ggc atg tat ctt gca gaa cgc ctt gta cag atc	48
Val Thr Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Val Gln Ile	
1 5 10 15	

ggg ctg aag cat cac ttc gcc gtg ggc ggc gac tac aat ctc gtt ctt	96
Gly Leu Lys His His Phe Ala Val Gly Gly Asp Tyr Asn Leu Val Leu	
20 25 30	

ctg gat cag ttg ctc ctc aac aag gac atg aaa cag atc tat tgc tgc	144
Leu Asp Gln Leu Leu Leu Asn Lys Asp Met Lys Gln Ile Tyr Cys Cys	
35 40 45	

aat gag ttg aac tgt ggc ttc agc gcg gaa ggc tac gcc cgt tct aac	192
Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ser Asn	
50 55 60	

ggg gct gcg gca gcg gtt gtc acc ttc agc gtt ggc gcc att tcc gcc	240
Gly Ala Ala Ala Ala Val Val Thr Phe Ser Val Gly Ala Ile Ser Ala	
65 70 75 80	

atg aac gcc ctc ggc ggc gcc tat gcc gaa aac ctg ccg gtt atc ctg	288
Met Asn Ala Leu Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu	
85 90 95	

att tcc ggc gcg ccc aac agc aat gat cag ggc aca ggt cat atc ctg	336
Ile Ser Gly Ala Pro Asn Ser Asn Asp Gln Gly Thr Gly His Ile Leu	

100	105	110	
cat cac aca atc ggc aag acg gat tac agc tac cag ctt gaa atg gcc His His Thr Ile Gly Lys Thr Asp Tyr Ser Tyr Gln Leu Glu Met Ala 115 120 125			384
cgt cag gtc acc tgt gcc gcc gaa agc att acc gac gct cac tcc gcc Arg Gln Val Thr Cys Ala Ala Glu Ser Ile Thr Asp Ala His Ser Ala 130 135 140			432
ccg gcc aag att gac cac gtc att cgc acg gcg ctg cgc gag cgt aag Pro Ala Lys Ile Asp His Val Ile Arg Thr Ala Leu Arg Glu Arg Lys 145 150 155 160			480
ccg gcc tat ctg gac atc gcg tgc aac att gcc tcc gag ccc tgc gtg Pro Ala Tyr Leu Asp Ile Ala Cys Asn Ile Ala Ser Glu Pro Cys Val 165 170 175			528
cgg cct ggc cct gtc agc agc ctg ctg tcc gag cct gaa atc gac cac Arg Pro Gly Pro Val Ser Ser Leu Leu Ser Glu Pro Glu Ile Asp His 180 185 190			576
acg agc ctg aag gcc gca gtg gac gcc acg gtt gcc ttg ctg aaa aat Thr Ser Leu Lys Ala Ala Val Asp Ala Thr Val Ala Leu Leu Lys Asn 195 200 205			624
cgg cca gcc ccc gtc atg ctg ctg ggc agc aag ctg cgg gcc gcc aac Arg Pro Ala Pro Val Met Leu Leu Gly Ser Lys Leu Arg Ala Ala Asn 210 215 220			672
gca ctg gcc gca acc gaa acg ctg gca gac aag ctg caa tgc gcg gtg Ala Leu Ala Ala Thr Glu Thr Leu Ala Asp Lys Leu Gln Cys Ala Val 225 230 235 240			720
acc atc atg gcg gcc gcg aaa ggc ttt ttc ccc gaa gac cac gcg ggt Thr Ile Met Ala Ala Ala Lys Gly Phe Phe Pro Glu Asp His Ala Gly 245 250 255			768
ttc cgc ggc ctg tac tgg ggc gaa gtc tcg aac ccc ggc gtg cag gaa Phe Arg Gly Leu Tyr Trp Gly Glu Val Ser Asn Pro Gly Val Gln Glu 260 265 270			816
ctg gtg gag acc tcc gac gca ctg ctg tgc atc gcc ccc gta ttc aac Leu Val Glu Thr Ser Asp Ala Leu Leu Cys Ile Ala Pro Val Phe Asn 275 280 285			864
gac tat tca aca gtc ggc tgg tcg ggc atg ccc aag ggc ccc aat gtg Asp Tyr Ser Thr Val Gly Trp Ser Gly Met Pro Lys Gly Pro Asn Val 290 295 300			912
att ctg gct gag ccc gac cgc gta acg gtc gat ggc cgc gcc tat gac Ile Leu Ala Glu Pro Asp Arg Val Thr Val Asp Gly Arg Ala Tyr Asp 305 310 315 320			960
ggc ttt acc ctg cgc gcc ttc ctg cag gct ctg gcg gaa aaa gcc ccc Gly Phe Thr Leu Arg Ala Phe Leu Gln Ala Leu Ala Glu Lys Ala Pro 325 330 335			1008
gcg cgc ccg gcc tcc gca cag aaa agc agc gtc ccg acg tgc tcg ctc			1056

Ala Arg Pro Ala Ser Ala Gln Lys Ser Ser Val Pro Thr Cys Ser Leu	
340	345
	350
acc gcg aca tcc gat gaa gcc ggt ctg acg aat gac gaa atc gtc cgt	1104
Thr Ala Thr Ser Asp Glu Ala Gly Leu Thr Asn Asp Glu Ile Val Arg	
355	360
	365
cat atc aac gcc ctg ctg aca tca aac acg acg ctg gtg gca gaa acc	1152
His Ile Asn Ala Leu Leu Thr Ser Asn Thr Thr Leu Val Ala Glu Thr	
370	375
	380
ggc gat tca tgg ttc aat gcc atg cgc atg acc ctg gcc ggt gcg cgc	1200
Gly Asp Ser Trp Phe Asn Ala Met Arg Met Thr Leu Ala Gly Ala Arg	
385	390
	395
gtg gaa ctg gaa atg cag tgg ggc cat atc ggc tgg tcc gtg ccc tcc	1248
Val Glu Leu Glu Met Gln Trp Gly His Ile Gly Trp Ser Val Pro Ser	
	405
	410
	415
gcg ttc ggc aat gcc atg ggc tgc cag gac cgc cag cat gtg gtg atg	1296
Ala Phe Gly Asn Ala Met Gly Ser Gln Asp Arg Gln His Val Val Met	
	420
	425
	430
gta ggc gat ggc tcc ttc cag ctt acc gcg cag gaa gtg gct cag atg	1344
Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Val Ala Gln Met	
	435
	440
	445
gtg cgc tac gaa ctg ccc gtc att atc ttt ctg atc aac aac cgt ggc	1392
Val Arg Tyr Glu Leu Pro Val Ile Ile Phe Leu Ile Asn Asn Arg Gly	
	450
	455
	460
tat gtc att gaa atc gcc att cat gac ggc ccg tac aac tat atc aag	1440
Tyr Val Ile Glu Ile Ala Ile His Asp Gly Pro Tyr Asn Tyr Ile Lys	
	465
	470
	475
	480
aac tgg gat tac gcc ggc ctg atg gaa gtc ttc aac gcc gga gaa ggc	1488
Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe Asn Ala Gly Glu Gly	
	485
	490
	495
cat gga ctt ggc ctg aaa gcc acc acc ccg aag gaa ctg aca gaa gcc	1536
His Gly Leu Gly Leu Lys Ala Thr Thr Pro Lys Glu Leu Thr Glu Ala	
	500
	505
	510
atc gcc agg gca aaa gcc aat acc cgc ggc ccg acg ctg atc gaa tgc	1584
Ile Ala Arg Ala Lys Ala Asn Thr Arg Gly Pro Thr Leu Ile Glu Cys	
	515
	520
	525
cag atc gac cgc acg gac tgc acg gat atg ctg gtt caa tgg ggc cgc	1632
Gln Ile Asp Arg Thr Asp Cys Thr Asp Met Leu Val Gln Trp Gly Arg	
	530
	535
	540
aag gtt gcc tca acc aac gcg cgc aag acc act ctg gcc tga	1674
Lys Val Ala Ser Thr Asn Ala Arg Lys Thr Thr Leu Ala	
	545
	550
	555

<210> 25

<211> 557

<212> PRT

<213> Acetobacter pasteurianus

<400> 25

Val Thr Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Val Gln Ile
 1 5 10 15

Gly Leu Lys His His Phe Ala Val Gly Gly Asp Tyr Asn Leu Val Leu
 20 25 30

Leu Asp Gln Leu Leu Leu Asn Lys Asp Met Lys Gln Ile Tyr Cys Cys
 35 40 45

Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ser Asn
 50 55 60

Gly Ala Ala Ala Ala Val Val Thr Phe Ser Val Gly Ala Ile Ser Ala
 65 70 75 80

Met Asn Ala Leu Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu
 85 90 95

Ile Ser Gly Ala Pro Asn Ser Asn Asp Gln Gly Thr Gly His Ile Leu
 100 105 110

His His Thr Ile Gly Lys Thr Asp Tyr Ser Tyr Gln Leu Glu Met Ala
 115 120 125

Arg Gln Val Thr Cys Ala Ala Glu Ser Ile Thr Asp Ala His Ser Ala
 130 135 140

Pro Ala Lys Ile Asp His Val Ile Arg Thr Ala Leu Arg Glu Arg Lys
 145 150 155 160

Pro Ala Tyr Leu Asp Ile Ala Cys Asn Ile Ala Ser Glu Pro Cys Val
 165 170 175

Arg Pro Gly Pro Val Ser Ser Leu Leu Ser Glu Pro Glu Ile Asp His
 180 185 190

Thr Ser Leu Lys Ala Ala Val Asp Ala Thr Val Ala Leu Leu Lys Asn
 195 200 205

Arg Pro Ala Pro Val Met Leu Leu Gly Ser Lys Leu Arg Ala Ala Asn
 210 215 220
 Ala Leu Ala Ala Thr Glu Thr Leu Ala Asp Lys Leu Gln Cys Ala Val
 225 230 235 240
 Thr Ile Met Ala Ala Ala Lys Gly Phe Phe Pro Glu Asp His Ala Gly
 245 250 255
 Phe Arg Gly Leu Tyr Trp Gly Glu Val Ser Asn Pro Gly Val Gln Glu
 260 265 270
 Leu Val Glu Thr Ser Asp Ala Leu Leu Cys Ile Ala Pro Val Phe Asn
 275 280 285
 Asp Tyr Ser Thr Val Gly Trp Ser Gly Met Pro Lys Gly Pro Asn Val
 290 295 300
 Ile Leu Ala Glu Pro Asp Arg Val Thr Val Asp Gly Arg Ala Tyr Asp
 305 310 315 320
 Gly Phe Thr Leu Arg Ala Phe Leu Gln Ala Leu Ala Glu Lys Ala Pro
 325 330 335
 Ala Arg Pro Ala Ser Ala Gln Lys Ser Ser Val Pro Thr Cys Ser Leu
 340 345 350
 Thr Ala Thr Ser Asp Glu Ala Gly Leu Thr Asn Asp Glu Ile Val Arg
 355 360 365
 His Ile Asn Ala Leu Leu Thr Ser Asn Thr Thr Leu Val Ala Glu Thr
 370 375 380
 Gly Asp Ser Trp Phe Asn Ala Met Arg Met Thr Leu Ala Gly Ala Arg
 385 390 395 400
 Val Glu Leu Glu Met Gln Trp Gly His Ile Gly Trp Ser Val Pro Ser
 405 410 415
 Ala Phe Gly Asn Ala Met Gly Ser Gln Asp Arg Gln His Val Val Met
 420 425 430
 Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Val Ala Gln Met

435

440

445

Val Arg Tyr Glu Leu Pro Val Ile Ile Phe Leu Ile Asn Asn Arg Gly
 450 455 460

Tyr Val Ile Glu Ile Ala Ile His Asp Gly Pro Tyr Asn Tyr Ile Lys
 465 470 475 480

Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe Asn Ala Gly Glu Gly
 485 490 495

His Gly Leu Gly Leu Lys Ala Thr Thr Pro Lys Glu Leu Thr Glu Ala
 500 505 510

Ile Ala Arg Ala Lys Ala Asn Thr Arg Gly Pro Thr Leu Ile Glu Cys
 515 520 525

Gln Ile Asp Arg Thr Asp Cys Thr Asp Met Leu Val Gln Trp Gly Arg
 530 535 540

Lys Val Ala Ser Thr Asn Ala Arg Lys Thr Thr Leu Ala
 545 550 555

<210> 26

<211> 32

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 26

atcttaatta atgtataccg ttggtatgta ct

32

<210> 27

<211> 34

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 27

tatgcggccg cttacgcttg tggtttgcga gagt

34

<210> 28

<211> 1671

<212> DNA

<213> Zymobacter palmae

<220>

<221> CDS

<222> (1)..(1671)

<223>

<400> 28

atg	tat	acc	gtt	ggt	atg	tac	ttg	gca	gaa	cgc	cta	gcc	cag	atc	ggc			48
Met	Tyr	Thr	Val	Gly	Met	Tyr	Leu	Ala	Glu	Arg	Leu	Ala	Gln	Ile	Gly			
1				5					10				15					

ctg	aaa	cac	cac	ttt	gcc	gtg	gcc	ggt	gac	tac	aac	ctg	gtg	ttg	ctt			96
Leu	Lys	His	His	Phe	Ala	Val	Ala	Gly	Asp	Tyr	Asn	Leu	Val	Leu	Leu			
			20					25					30					

gat	cag	ctc	ctg	ctg	aac	aaa	gac	atg	gag	cag	gtc	tac	tgc	tgt	aac			144
Asp	Gln	Leu	Leu	Leu	Asn	Lys	Asp	Met	Glu	Gln	Val	Tyr	Cys	Cys	Asn			
		35				40						45						

gaa	ctt	aac	tgc	ggc	ttt	agc	gcc	gaa	ggt	tac	gct	cgt	gca	cgt	ggt			192
Glu	Leu	Asn	Cys	Gly	Phe	Ser	Ala	Glu	Gly	Tyr	Ala	Arg	Ala	Arg	Gly			
	50					55				60								

gcc	gcc	gct	gcc	atc	gtc	acg	ttc	agc	gta	ggt	gct	atc	tct	gca	atg			240
Ala	Ala	Ala	Ala	Ile	Val	Thr	Phe	Ser	Val	Gly	Ala	Ile	Ser	Ala	Met			
65					70					75					80			

aac	gcc	atc	ggt	ggc	gcc	tat	gca	gaa	aac	ctg	ccg	gtc	atc	ctg	atc			288
Asn	Ala	Ile	Gly	Gly	Ala	Tyr	Ala	Glu	Asn	Leu	Pro	Val	Ile	Leu	Ile			
			85						90					95				

tct	ggc	tca	ccg	aac	acc	aat	gac	tac	ggc	aca	ggc	cac	atc	ctg	cac			336
Ser	Gly	Ser	Pro	Asn	Thr	Asn	Asp	Tyr	Gly	Thr	Gly	His	Ile	Leu	His			
			100					105					110					

cac	acc	att	ggt	act	act	gac	tat	aac	tat	cag	ctg	gaa	atg	gta	aaa			384
His	Thr	Ile	Gly	Thr	Thr	Asp	Tyr	Asn	Tyr	Gln	Leu	Glu	Met	Val	Lys			

115	120	125	
cac gtt acc tgc gca cgt gaa agc atc gtt tct gcc gaa gaa gca ccg His Val Thr Cys Ala Arg Glu Ser Ile Val Ser Ala Glu Glu Ala Pro 130 135 140			432
gca aaa atc gac cac gtc atc cgt acg gct cta cgt gaa cgc aaa ccg Ala Lys Ile Asp His Val Ile Arg Thr Ala Leu Arg Glu Arg Lys Pro 145 150 155 160			480
gct tat ctg gaa atc gca tgc aac gtc gct ggc gct gaa tgt gtt cgt Ala Tyr Leu Glu Ile Ala Cys Asn Val Ala Gly Ala Glu Cys Val Arg 165 170 175			528
ccg ggc ccg atc aat agc ctg ctg cgt gaa ctc gaa gtt gac cag acc Pro Gly Pro Ile Asn Ser Leu Leu Arg Glu Leu Glu Val Asp Gln Thr 180 185 190			576
agt gtc act gcc gct gta gat gcc gcc gta gaa tgg ctg cag gac cgc Ser Val Thr Ala Ala Val Asp Ala Ala Val Glu Trp Leu Gln Asp Arg 195 200 205			624
cag aac gtc gtc atg ctg gtc ggt agc aaa ctg cgt gcc gct gcc gct Gln Asn Val Val Met Leu Val Gly Ser Lys Leu Arg Ala Ala Ala Ala 210 215 220			672
gaa aaa cag gct gtt gcc cta gcg gac cgc ctg ggc tgc gct gtc acg Glu Lys Gln Ala Val Ala Leu Ala Asp Arg Leu Gly Cys Ala Val Thr 225 230 235 240			720
atc atg gct gcc gaa aaa ggc ttc ttc ccg gaa gat cat ccg aac ttc Ile Met Ala Ala Glu Lys Gly Phe Phe Pro Glu Asp His Pro Asn Phe 245 250 255			768
cgc ggc ctg tac tgg ggt gaa gtc agc tcc gaa ggt gca cag gaa ctg Arg Gly Leu Tyr Trp Gly Glu Val Ser Ser Glu Gly Ala Gln Glu Leu 260 265 270			816
gtt gaa aac gcc gat gcc atc ctg tgt ctg gca ccg gta ttc aac gac Val Glu Asn Ala Asp Ala Ile Leu Cys Leu Ala Pro Val Phe Asn Asp 275 280 285			864
tat gct acc gtt ggc tgg aac tcc tgg ccg aaa ggc gac aat gtc atg Tyr Ala Thr Val Gly Trp Asn Ser Trp Pro Lys Gly Asp Asn Val Met 290 295 300			912
gtc atg gac acc gac cgc gtc act ttc gca gga cag tcc ttc gaa ggt Val Met Asp Thr Asp Arg Val Thr Phe Ala Gly Gln Ser Phe Glu Gly 305 310 315 320			960
ctg tca ttg agc acc ttc gcc gca gca ctg gct gag aaa gca cct tct Leu Ser Leu Ser Thr Phe Ala Ala Ala Leu Ala Glu Lys Ala Pro Ser 325 330 335			1008
cgc ccg gca acg act caa ggc act caa gca ccg gta ctg ggt att gag Arg Pro Ala Thr Gln Gly Thr Gln Ala Pro Val Leu Gly Ile Glu 340 345 350			1056
gcc gca gag ccc aat gca ccg ctg acc aat gac gaa atg acg cgt cag			1104

Ala Ala Glu Pro Asn Ala Pro Leu Thr Asn Asp Glu Met Thr Arg Gln	355	360	365	
atc cag tcg ctg atc act tcc gac act act ctg aca gca gaa aca ggt				1152
Ile Gln Ser Leu Ile Thr Ser Asp Thr Thr Leu Thr Ala Glu Thr Gly	370	375	380	
gac tct tgg ttc aac gct tct cgc atg ccg att cct ggc ggt gct cgt				1200
Asp Ser Trp Phe Asn Ala Ser Arg Met Pro Ile Pro Gly Gly Ala Arg	385	390	395	400
gtc gaa ctg gaa atg caa tgg ggt cat atc ggt tgg tcc gta cct tct				1248
Val Glu Leu Glu Met Gln Trp Gly His Ile Gly Trp Ser Val Pro Ser		405	410	415
gca ttc ggt aac gcc gtt ggt tct ccg gag cgt cgc cac atc atg atg				1296
Ala Phe Gly Asn Ala Val Gly Ser Pro Glu Arg Arg His Ile Met Met	420		425	430
gtc ggt gat ggc tct ttc cag ctg act gct caa gaa gtt gct cag atg				1344
Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Val Ala Gln Met		435	440	445
atc cgc tat gaa atc ccg gtc atc atc ttc ctg atc aac aac cgc ggt				1392
Ile Arg Tyr Glu Ile Pro Val Ile Ile Phe Leu Ile Asn Asn Arg Gly	450	455	460	
tac gtc atc gaa atc gct atc cat gac ggc cct tac aac tac atc aaa				1440
Tyr Val Ile Glu Ile Ala Ile His Asp Gly Pro Tyr Asn Tyr Ile Lys	465	470	475	480
aac tgg aac tac gct ggc ctg atc gac gtc ttc aat gac gaa gat ggt				1488
Asn Trp Asn Tyr Ala Gly Leu Ile Asp Val Phe Asn Asp Glu Asp Gly		485	490	495
cat ggc ctg ggt ctg aaa gct tct act ggt gca gaa cta gaa ggc gct				1536
His Gly Leu Gly Leu Lys Ala Ser Thr Gly Ala Glu Leu Glu Gly Ala		500	505	510
atc aag aaa gca ctc gac aat cgt cgc ggt ccg acg ctg atc gaa tgt				1584
Ile Lys Lys Ala Leu Asp Asn Arg Arg Gly Pro Thr Leu Ile Glu Cys		515	520	525
aac atc gct cag gac gac tgc act gaa acc ctg att gct tgg ggt aaa				1632
Asn Ile Ala Gln Asp Asp Cys Thr Glu Thr Leu Ile Ala Trp Gly Lys	530	535	540	
cgt gta gca gct acc aac tct cgc aaa cca caa gcg taa				1671
Arg Val Ala Ala Thr Asn Ser Arg Lys Pro Gln Ala	545	550	555	
<210> 29				
<211> 556				
<212> PRT				
<213> Zymobacter palmae				

<400> 29

Met Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Ala Gln Ile Gly
 1 5 10 15

Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu Leu
 20 25 30

Asp Gln Leu Leu Leu Asn Lys Asp Met Glu Gln Val Tyr Cys Cys Asn
 35 40 45

Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ala Arg Gly
 50 55 60

Ala Ala Ala Ala Ile Val Thr Phe Ser Val Gly Ala Ile Ser Ala Met
 65 70 75 80

Asn Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu Ile
 85 90 95

Ser Gly Ser Pro Asn Thr Asn Asp Tyr Gly Thr Gly His Ile Leu His
 100 105 110

His Thr Ile Gly Thr Thr Asp Tyr Asn Tyr Gln Leu Glu Met Val Lys
 115 120 125

His Val Thr Cys Ala Arg Glu Ser Ile Val Ser Ala Glu Glu Ala Pro
 130 135 140

Ala Lys Ile Asp His Val Ile Arg Thr Ala Leu Arg Glu Arg Lys Pro
 145 150 155 160

Ala Tyr Leu Glu Ile Ala Cys Asn Val Ala Gly Ala Glu Cys Val Arg
 165 170 175

Pro Gly Pro Ile Asn Ser Leu Leu Arg Glu Leu Glu Val Asp Gln Thr
 180 185 190

Ser Val Thr Ala Ala Val Asp Ala Ala Val Glu Trp Leu Gln Asp Arg
 195 200 205

Gln Asn Val Val Met Leu Val Gly Ser Lys Leu Arg Ala Ala Ala Ala
 210 215 220

Glu Lys Gln Ala Val Ala Leu Ala Asp Arg Leu Gly Cys Ala Val Thr
 225 230 235 240

Ile Met Ala Ala Glu Lys Gly Phe Phe Pro Glu Asp His Pro Asn Phe
 245 250 255

Arg Gly Leu Tyr Trp Gly Glu Val Ser Ser Glu Gly Ala Gln Glu Leu
 260 265 270

Val Glu Asn Ala Asp Ala Ile Leu Cys Leu Ala Pro Val Phe Asn Asp
 275 280 285

Tyr Ala Thr Val Gly Trp Asn Ser Trp Pro Lys Gly Asp Asn Val Met
 290 295 300

Val Met Asp Thr Asp Arg Val Thr Phe Ala Gly Gln Ser Phe Glu Gly
 305 310 315 320

Leu Ser Leu Ser Thr Phe Ala Ala Ala Leu Ala Glu Lys Ala Pro Ser
 325 330 335

Arg Pro Ala Thr Thr Gln Gly Thr Gln Ala Pro Val Leu Gly Ile Glu
 340 345 350

Ala Ala Glu Pro Asn Ala Pro Leu Thr Asn Asp Glu Met Thr Arg Gln
 355 360 365

Ile Gln Ser Leu Ile Thr Ser Asp Thr Thr Leu Thr Ala Glu Thr Gly
 370 375 380

Asp Ser Trp Phe Asn Ala Ser Arg Met Pro Ile Pro Gly Gly Ala Arg
 385 390 395 400

Val Glu Leu Glu Met Gln Trp Gly His Ile Gly Trp Ser Val Pro Ser
 405 410 415

Ala Phe Gly Asn Ala Val Gly Ser Pro Glu Arg Arg His Ile Met Met
 420 425 430

Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Val Ala Gln Met
 435 440 445

Ile Arg Tyr Glu Ile Pro Val Ile Ile Phe Leu Ile Asn Asn Arg Gly

450

455

460

Tyr Val Ile Glu Ile Ala Ile His Asp Gly Pro Tyr Asn Tyr Ile Lys
 465 470 475 480

Asn Trp Asn Tyr Ala Gly Leu Ile Asp Val Phe Asn Asp Glu Asp Gly
 485 490 495

His Gly Leu Gly Leu Lys Ala Ser Thr Gly Ala Glu Leu Glu Gly Ala
 500 505 510

Ile Lys Lys Ala Leu Asp Asn Arg Arg Gly Pro Thr Leu Ile Glu Cys
 515 520 525

Asn Ile Ala Gln Asp Asp Cys Thr Glu Thr Leu Ile Ala Trp Gly Lys
 530 535 540

Arg Val Ala Ala Thr Asn Ser Arg Lys Pro Gln Ala
 545 550 555

<210> 30

<211> 32

<212> DNA

<213> artificial sequence

<400> 30
 ctattaatta atggcttcgg tacacggcac ca

32

<210> 31

<211> 34

<212> DNA

<213> artificial sequence

<400> 31
 tatgcggcgc cttacttcac cgggcttacg gtgc

34

<210> 32

<211> 1587

<212> DNA

<213> *Pseudomonas putida*

<220>

<221> CDS

<222> (1)..(1584)

<223>

<400> 32

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Met Ala Ser Val His Gly Thr Thr Tyr Glu Leu Leu Arg Arg Gln Gly	
1 5 10 15	
atc gat acg gtc ttc ggc aat cct ggc tcg aac gag ctc ccg ttt ttg	96
Ile Asp Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu	
20 25 30	
aag gac ttt cca gag gac ttt cga tac atc ctg gct ttg cag gaa gcg	144
Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Ala Leu Gln Glu Ala	
35 40 45	
tgt gtg gtg ggc att gca gac ggc tat gcg caa gcc agt cgg aag ccg	192
Cys Val Val Gly Ile Ala Asp Gly Tyr Ala Gln Ala Ser Arg Lys Pro	
50 55 60	
gct ttc att aac ctg cat tct gct gct ggt acc ggc aat gct atg ggt	240
Ala Phe Ile Asn Leu His Ser Ala Ala Gly Thr Gly Asn Ala Met Gly	
65 70 75 80	
gca ctc agt aac gcc tgg aac tca cat tcc ccg ctg atc gtc act gcc	288
Ala Leu Ser Asn Ala Trp Asn Ser His Ser Pro Leu Ile Val Thr Ala	
85 90 95	
ggc cag cag acc agg gcg atg att ggc gtt gaa gct ctg ctg acc aac	336
Gly Gln Gln Thr Arg Ala Met Ile Gly Val Glu Ala Leu Leu Thr Asn	
100 105 110	
gtc gat gcc gcc aac ctg cca cga cca ctt gtc aaa tgg agc tac gag	384
Val Asp Ala Ala Asn Leu Pro Arg Pro Leu Val Lys Trp Ser Tyr Glu	
115 120 125	
ccc gca agc gca gca gaa gtc cct cat gcg atg agc agg gct atc cat	432
Pro Ala Ser Ala Ala Glu Val Pro His Ala Met Ser Arg Ala Ile His	
130 135 140	
atg gca agc atg gcg cca caa ggc cct gtc tat ctt tcg gtg cca tat	480
Met Ala Ser Met Ala Pro Gln Gly Pro Val Tyr Leu Ser Val Pro Tyr	
145 150 155 160	
gac gat tgg gat aag gat gct gat cct cag tcc cac cac ctt ttt gat	528
Asp Asp Trp Asp Lys Asp Ala Asp Pro Gln Ser His His Leu Phe Asp	

165	170	175	
cgc cat gtc agt tca tca gta cgc ctg aac gac cag gat ctc gat att Arg His Val Ser Ser Ser Val Arg Leu Asn Asp Gln Asp Leu Asp Ile 180 185 190			576
ctg gtg aaa gct ctc aac agc gca tcc aac ccg gcg atc gtc ctg ggc Leu Val Lys Ala Leu Asn Ser Ala Ser Asn Pro Ala Ile Val Leu Gly 195 200 205			624
ccg gac gtc gac gca gca aat gcg aac gca gac tgc gtc atg ttg gcc Pro Asp Val Asp Ala Ala Asn Ala Asn Ala Asp Cys Val Met Leu Ala 210 215 220			672
gaa cgc ctc aaa gct ccg gtt tgg gtt gcg cca tcc gct cca cgc tgc Glu Arg Leu Lys Ala Pro Val Trp Val Ala Pro Ser Ala Pro Arg Cys 225 230 235 240			720
cca ttc cct acc cgt cat cct tgc ttc cgt gga ttg atg cca gct ggc Pro Phe Pro Thr Arg His Pro Cys Phe Arg Gly Leu Met Pro Ala Gly 245 250 255			768
atc gca gcg att tct cag ctg ctc gaa ggt cac gat gtg gtt ttg gta Ile Ala Ala Ile Ser Gln Leu Leu Glu Gly His Asp Val Val Leu Val 260 265 270			816
atc ggc gct cca gtg ttc cgt tac cac caa tac gac cca ggt caa tat Ile Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Asp Pro Gly Gln Tyr 275 280 285			864
ctc aaa cct ggc acg cga ttg att tcg gtg acc tgc gac ccg ctc gaa Leu Lys Pro Gly Thr Arg Leu Ile Ser Val Thr Cys Asp Pro Leu Glu 290 295 300			912
gct gca cgc gcg cca atg ggc gat gcg atc gtg gca gac att ggt gcg Ala Ala Arg Ala Pro Met Gly Asp Ala Ile Val Ala Asp Ile Gly Ala 305 310 315 320			960
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cca act gca gct ccg gaa ccc gcg aag gtt gac caa gac gct ggc cga Pro Thr Ala Ala Pro Glu Pro Ala Lys Val Asp Gln Asp Ala Gly Arg 340 345 350			1056
ctt cac cca gag aca gtg ttc gac aca ctg aac gac atg gcc ccg gag Leu His Pro Glu Thr Val Phe Asp Thr Leu Asn Asp Met Ala Pro Glu 355 360 365			1104
aat gcg att tac ctg aac gag tcg act tca acg acc gcc caa atg tgg Asn Ala Ile Tyr Leu Asn Glu Ser Thr Ser Thr Thr Ala Gln Met Trp 370 375 380			1152
cag cgc ctg aac atg cgc aac cct ggt agc tac tac ttc tgt gca gct Gln Arg Leu Asn Met Arg Asn Pro Gly Ser Tyr Tyr Phe Cys Ala Ala 385 390 395 400			1200
ggc gga ctg ggc ttc gcc ctg cct gca gca att ggc gtt caa ctc gca			1248

Gly Gly Leu Gly Phe Ala Leu Pro Ala Ala Ile Gly Val Gln Leu Ala
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 gaa ccc gag cga caa gtc atc gcc gtc att ggc gac gga tcg gcg aac 1296
 Glu Pro Glu Arg Gln Val Ile Ala Val Ile Gly Asp Gly Ser Ala Asn
 420 425 430
 tac agc att agt gcg ttg tgg act gca gct cag tac aac atc ccc act 1344
 Tyr Ser Ile Ser Ala Leu Trp Thr Ala Ala Gln Tyr Asn Ile Pro Thr
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 atc ttc gtg atc atg aac aac ggc acc tac ggt gcg ttg cga tgg ttt 1392
 Ile Phe Val Ile Met Asn Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
 450 455 460
 gcc ggc gtt ctc gaa gca gaa aac gtt cct ggg ctg gat gtg cca ggg 1440
 Ala Gly Val Leu Glu Ala Glu Asn Val Pro Gly Leu Asp Val Pro Gly
 465 470 475 480
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 Ile Asp Phe Arg Ala Leu Ala Lys Gly Tyr Gly Val Gln Ala Leu Lys
 485 490 495
 gcc gac aac ctt gag cag ctc aag ggt tcg cta caa gaa gcg ctt tct 1536
 Ala Asp Asn Leu Glu Gln Leu Lys Gly Ser Leu Gln Glu Ala Leu Ser
 500 505 510
 gcc aaa ggc ccg gta ctt atc gaa gta agc acc gta agc ccg gtg aag 1584
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 tga 1587

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 35 40 45
 Cys Val Val Gly Ile Ala Asp Gly Tyr Ala Gln Ala Ser Arg Lys Pro

45/46

Leu Lys Pro Gly Thr Arg Leu Ile Ser Val Thr Cys Asp Pro Leu Glu
 290 295 300

Ala Ala Arg Ala Pro Met Gly Asp Ala Ile Val Ala Asp Ile Gly Ala
 305 310 315 320

Met Ala Ser Ala Leu Ala Asn Leu Val Glu Glu Ser Ser Arg Gln Leu
 325 330 335

Pro Thr Ala Ala Pro Glu Pro Ala Lys Val Asp Gln Asp Ala Gly Arg
 340 345 350

Leu His Pro Glu Thr Val Phe Asp Thr Leu Asn Asp Met Ala Pro Glu
 355 360 365

Asn Ala Ile Tyr Leu Asn Glu Ser Thr Ser Thr Thr Ala Gln Met Trp
 370 375 380

Gln Arg Leu Asn Met Arg Asn Pro Gly Ser Tyr Tyr Phe Cys Ala Ala
 385 390 395 400

Gly Gly Leu Gly Phe Ala Leu Pro Ala Ala Ile Gly Val Gln Leu Ala
 405 410 415

Glu Pro Glu Arg Gln Val Ile Ala Val Ile Gly Asp Gly Ser Ala Asn
 420 425 430

Tyr Ser Ile Ser Ala Leu Trp Thr Ala Ala Gln Tyr Asn Ile Pro Thr
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Ile Phe Val Ile Met Asn Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
 450 455 460

Ala Gly Val Leu Glu Ala Glu Asn Val Pro Gly Leu Asp Val Pro Gly
 465 470 475 480

Ile Asp Phe Arg Ala Leu Ala Lys Gly Tyr Gly Val Gln Ala Leu Lys
 485 490 495

Ala Asp Asn Leu Glu Gln Leu Lys Gly Ser Leu Gln Glu Ala Leu Ser
 500 505 510

Ala Lys Gly Pro Val Leu Ile Glu Val Ser Thr Val Ser Pro Val Lys
 515 520 525